Data structures in R

The base structures

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Preliminaries to find data (and images for these slides)

```r
# A little function that just concatenates paths (as strings)
# to produce a "path" to some file/directory
path_concat <- function(path1,
                        path2,
                        sep="/") {
    paste(path1, path2, sep = sep)
    }

# Note that you might have to give a different value
# for the directory separator (e.g. sep = "\" on Windows?)
#
# Here's where my course files are on my machine
coursesDirectory <- "/Users/rwoldford/Documents/Admin/courses/"
#
# Use path_concat() to produce new paths to sub-directories.
# For example:
EDA <- path_concat(coursesDirectory, "STAT\ 847")
dataDirectory <- path_concat(EDA, "data")
imageDirectory <- path_concat(EDA, "img")
```

Data structures in R

The base data structures in `R`:

dimensionality	homogeneous contents	heterogeneous contents
1d	Atomic vector	List
2d	Matrix	Data frame
nd	Array	

Note there are no scalar or 0-dimensional data structures. Instead these are `1d` data structures having a single element.

There are also three different types of object-oriented programming systems in `R` (**S3**, **S4**, and **reference classes**) which can be used to construct more complex data types.

The function `str()` can be used to reveal the contents of any `R` data structure.

Data structures in `R` *– Vectors*

The basic data structure is a “vector”

Two kinds: atomic vectors and lists.

Three properties:

- its type, `typeof()`
- the number of elements it has, `length()`
- a place for arbitrary additional properties, `attributes()`

Elements of an **atomic vector** must all be of the **same** type.

Elements of a **list** can be of different types.

Constructors: `c()` for atomic vectors, `list()` for lists.

tests: `is.atomic()` and `is.list()`.

Data structures in R – `c()` constructing atomic vectors

Atomic vectors are constructed using `c()` (c for "combine")

```
x <- c(1, 2, 3)
x
```

```
## [1] 1 2 3
```

```
is.atomic(x)
```

```
## [1] TRUE
```

```
is.list(x)
```

```
## [1] FALSE
```

Atomic vectors are always "flat"

```
y <- c(x, x, 4, 5, 6)
y
```

```
## [1] 1 2 3 1 2 3 4 5 6
```

```
c(y, c(7, 8, x, 9, c(10, 11)))
```

```
##  [1]  1  2  3  1  2  3  4  5  6  7  8  1  2  3  9 10 11
```

Data structures in R – c() constructing atomic vectors

Elements of an atomic vector are accesssed using the [] operator (see ?"[")

```
x <- c("a", "b", "c", "d", "e", "f")
x[3]
```

```
## [1] "c"
```

```
x[c(1,3,5)]
```

```
## [1] "a" "c" "e"
```

And set with the same function

```
x[1] <- "EH"
x
```

```
## [1] "EH" "b"  "c"  "d"  "e"  "f"
```

```
x[c(3,5)] <- c("third", "fifth")
x
```

```
## [1] "EH"    "b"     "third" "d"     "fifth" "f"
```

Data structures in R – `double` precision numeric vectors

```r
x <- c(1, 2, 3)
length(x)
```

```
## [1] 3
```

```r
typeof(x)
```

```
## [1] "double"
```

```r
attributes(x)
```

```
## NULL
```

```r
is.atomic(x)
```

```
## [1] TRUE
```

```r
is.numeric(x)
```

```
## [1] TRUE
```

```r
is.double(x)
```

```
## [1] TRUE
```

Data structures in R – integer numeric vectors

```
x <- c(1L, 20L, 3L)  # "longs"
length(x)
```

```
## [1] 3
```

```
typeof(x)
```

```
## [1] "integer"
```

```
attributes(x)
```

```
## NULL
```

```
is.atomic(x)
```

```
## [1] TRUE
```

```
is.numeric(x)
```

```
## [1] TRUE
```

```
is.integer(x)
```

```
## [1] TRUE
```

Data structures in R – `logical` vectors

```r
x <- c(T, F, TRUE, T, FALSE, T)
length(x)
```

```
## [1] 6
```

```r
typeof(x)
```

```
## [1] "logical"
```

```r
attributes(x)
```

```
## NULL
```

```r
is.atomic(x)
```

```
## [1] TRUE
```

```r
is.numeric(x)
```

```
## [1] FALSE
```

```r
is.logical(x)
```

```
## [1] TRUE
```

Data structures in R – `character` vectors

```r
x <- c("Now", "is the time", "for", "all")
length(x)
```

```
## [1] 4
```

```r
typeof(x)
```

```
## [1] "character"
```

```r
attributes(x)
```

```
## NULL
```

```r
is.atomic(x)
```

```
## [1] TRUE
```

```r
is.numeric(x)
```

```
## [1] FALSE
```

```r
is.character(x)
```

```
## [1] TRUE
```

Data structures in R – type contagion

From least to most flexible vector types are: `logical`, `integer`, `double`, and `character`.

Elements are coerced to be of the **same** type (the most flexible).

```r
typeof(c(FALSE, T))
```

```
## [1] "logical"
```

```r
typeof(c(FALSE, T, 2L))
```

```
## [1] "integer"
```

```r
typeof(c(FALSE, T, 2L, 3))
```

```
## [1] "double"
```

```r
typeof(c(FALSE, T, 2L, 3, "four"))
```

```
## [1] "character"
```

```r
c(FALSE, T, 2L, 3, "four")
```

```
## [1] "FALSE" "TRUE"  "2"     "3"     "four"
```

All elements are automatically coerced to be strings.

Data structures in R – coercion

Can force the coercion using `as.numeric()`, `as.double()`, `as.integer()`, or `as.logical()`

```r
as.numeric(c(FALSE, T, TRUE, F, F))
```

```
## [1] 0 1 1 0 0
```

```r
as.double(c(FALSE, T, TRUE, F, F))
```

```
## [1] 0 1 1 0 0
```

```r
as.integer(c(FALSE, T, TRUE, F, F))
```

```
## [1] 0 1 1 0 0
```

```r
as.character(c(FALSE, T, TRUE, F, F))
```

```
## [1] "FALSE" "TRUE"  "TRUE"  "FALSE" "FALSE"
```

```r
as.logical(c(0, 1, 2.3, 4.5, 6))
```

```
## [1] FALSE  TRUE  TRUE  TRUE  TRUE
```

Note that many functions will force their argument to the required `type`.

E.g. `sum()` forces its argument to be numeric, logical operators `&`, `|`, etc. force theirs to be `logical`.

Data structures in R – coercion

Forcing coercion can result in the loss of information and can give some strange answers:

```r
as.numeric(c(FALSE, T, 2L, 3))
```

```
## [1] 0 1 2 3
```

```r
as.numeric(c(FALSE, T, 2L, 3, "four"))
```

```
## Warning: NAs introduced by coercion

## [1] NA NA  2  3 NA
```

```r
as.numeric(c(as.numeric(c(FALSE, T, 2L, 3)), "four"))
```

```
## Warning: NAs introduced by coercion

## [1]  0  1  2  3 NA
```

Note that warnings are given.

Data structures in R – vectors

Can also produce a vector (possibly to be modified later) by specifying its type (mode) and length:

```
x <- vector(mode = "double", length = 3)
x
```

```
## [1] 0 0 0
```

```
y <- vector(mode = "logical", length = 3)
y
```

```
## [1] FALSE FALSE FALSE
```

```
z <- vector(mode = "character", length = 3)
z
```

```
## [1] "" "" ""
```

Data structures in R – Lists

Elements of lists can be of any type:

```
x <- list("a", c(2, 3, 4), c(T,F), c("b", "c", "d", 56))
x
```

```
## [[1]]
## [1] "a"
##
## [[2]]
## [1] 2 3 4
##
## [[3]]
## [1]  TRUE FALSE
##
## [[4]]
## [1] "b"  "c"  "d"  "56"
```

```
str(x)
```

```
## List of 4
##  $ : chr "a"
##  $ : num [1:3] 2 3 4
##  $ : logi [1:2] TRUE FALSE
##  $ : chr [1:4] "b" "c" "d" "56"
```

```
attributes(x)
```

```
## NULL
```

Note the **double** square brackets now appearing!

Data structures in R – Lists

Elements of lists can accessed in a few ways:

```
x[2]
```

```
## [[1]]
## [1] 2 3 4
```

```
typeof(x[2])
```

```
## [1] "list"
```

```
length(x[2])
```

```
## [1] 1
```

```
x[[2]]
```

```
## [1] 2 3 4
```

```
typeof(x[[2]])
```

```
## [1] "double"
```

And can be created using `vector()`, default elements being `NULL` (being an “empty” vector)

```
vector(mode = "list", length = 3)[[1]]
```

```
## NULL
```

Data structures in R – Lists are recursive

```r
x <- list("one", 2)
is.recursive(x)
```

```
## [1] TRUE
```

Lists can be arbitrarily recursive:

```r
y <- list(x, list(3, x))
is.recursive(y)
```

```
## [1] TRUE
```

```r
str(y)
```

```
## List of 2
##  $ :List of 2
##   ..$ : chr "one"
##   ..$ : num 2
##  $ :List of 2
##   ..$ : num 3
##   ..$ :List of 2
##   .. ..$ : chr "one"
##   .. ..$ : num 2
```

Data structures in R – Vectors can have named components

Atomic vectors

```
x <- c(a=3, b=4, 5)
x
```

```
## a b
## 3 4 5
```

```
names(x)
```

```
## [1] "a" "b" ""
```

```
x["a"]
```

```
## a
## 3
```

```
attributes(x)
```

```
## $names
## [1] "a" "b" ""
```

Data structures in R – Vectors can have named components

Lists (or “recursive vectors”)

```r
x <- list(a=c(1,2,3), b=4, 5)
str(x)
```

```
## List of 3
##  $ a: num [1:3] 1 2 3
##  $ b: num 4
##  $  : num 5
```

```r
x["b"]
```

```
## $b
## [1] 4
```

```r
x$b
```

```
## [1] 4
```

```r
names(x)
```

```
## [1] "a" "b" ""
```

Data structures in `R` *– Lists as general data structures*

Lists (handy with named components) can be used to create more general structures. For example,

```
# data frames:
is.list(cars)
```

```
## [1] TRUE
```

```
names(cars)
```

```
## [1] "speed" "dist"
```

```
# results of functions
fit <- lm(dist ~ speed, data = cars)
is.list(fit)
```

```
## [1] TRUE
```

```
names(fit)
```

```
##  [1] "coefficients"  "residuals"     "effects"       "rank"
##  [5] "fitted.values" "assign"        "qr"            "df.residual"
##  [9] "xlevels"       "call"          "terms"         "model"
```

Data structures in R – Lists to atomic vectors

Sometimes it can be handy to change a list to an atomic vector:

```r
x <- list(a = 1, b = c(2, 3, 4), c = list(e = c(5, 6), f = c(7, 8, 9)))
str(x)
```

```
## List of 3
##  $ a: num 1
##  $ b: num [1:3] 2 3 4
##  $ c:List of 2
##   ..$ e: num [1:2] 5 6
##   ..$ f: num [1:3] 7 8 9
```

```r
y <- unlist(x)
is.list(y)
```

```
## [1] FALSE
```

```r
y
```

```
##    a   b1   b2   b3 c.e1 c.e2 c.f1 c.f2 c.f3
##    1    2    3    4    5    6    7    8    9
```

```r
names(y)
```

```
## [1] "a"    "b1"   "b2"   "b3"   "c.e1" "c.e2" "c.f1" "c.f2" "c.f3"
```

Data structures in R – attributes

Additional information can be added to any `R` object as one or more attributes.

- these are very much like a property list (or plist) in other languages.

```
y
```

```
##    a   b1   b2   b3 c.e1 c.e2 c.f1 c.f2 c.f3
##    1    2    3    4    5    6    7    8    9
```

```
names(y)
```

```
## [1] "a"    "b1"   "b2"   "b3"   "c.e1" "c.e2" "c.f1" "c.f2" "c.f3"
```

```
# introduce a specific attribute
attr(y, "originalNames") <- c("a", "b", "c", "d", "e", "f")
attr(y, "originalNames")
```

```
## [1] "a" "b" "c" "d" "e" "f"
```

which provides a simple cache of the component names from the original list hierarchy.

Data structures in R – attributes

Using `attr()` to set a specific named attribute on the object modifies that object:

```
tau <- 2 * pi
attr(tau, "description") <-  "Twice pi"
attributes(tau)
```

```
## $description
## [1] "Twice pi"
```

`structure()` is similar but returns a copy:

```
TwoPi <- structure(tau, description  = "Two times pi")
attributes(TwoPi)
```

```
## $description
## [1] "Two times pi"
```

```
# TwoPi is a different object having the same value as tau
# which can be checked here since it is just a numeric vector
tau == TwoPi
```

```
## [1] TRUE
```

Data structures in R – attributes

Of course, assigning a value to `attributes()` will change all attributes on that object.

```r
attributes(tau)
```

```
## $description
## [1] "Twice pi"
```

```r
attributes(tau) <- list(constant = "tau")
```

and we have lost the previous attributes.

```r
attributes(tau)
```

```
## $constant
## [1] "tau"
```

Data structures in R *– factors*

A factor is a special kind of atomic vector having class `factor` and an attribute called `levels`. A factor is typically used to represent a categorical variate having a fixed, finite, and known set of values. The possible values are assigned to the factor levels.

```r
treatment <- factor(c("a", "b", "b", "b", "a", "c", "c", "a", "b"))
levels(treatment)
```

```
## [1] "a" "b" "c"
```

```r
table(treatment)
```

```
## treatment
## a b c
## 3 4 2
```

```r
# levels are fixed
treatment[3] <- "d"
```

```
## Warning in `[<-.factor`(`*tmp*`, 3, value = "d"): invalid factor level, NA
## generated
```

```r
treatment
```

```
## [1] a    b    <NA> b    a    c    c    a    b
## Levels: a b c
```

Data structures in R – factors

A factor is an atomic vector,

```r
is.atomic(treatment)
```

```
## [1] TRUE
```

```r
typeof(treatment)
```

```
## [1] "integer"
```

of type `integer` having a `length` and `attributes`

```r
length(treatment)
```

```
## [1] 9
```

```r
attributes(treatment)
```

```
## $levels
## [1] "a" "b" "c"
##
## $class
## [1] "factor"
```

Data structures in R – factors

These attributes can be accessed via two functions

```
levels(treatment)
```

```
## [1] "a" "b" "c"
```

```
class(treatment)
```

```
## [1] "factor"
```

Data structures in R – factors

All factor levels need to be known, but need not appear:

```r
answer <- factor(c(1, 2, 1, 1, 2, 2, 1, 1, 2), levels = c(1, 2, 3))
table(answer)
```

```
## answer
## 1 2 3
## 5 4 0
```

Again, `answer` is a factor and not

```r
is.integer(answer)
```

```
## [1] FALSE
```

Data structures in R – factors

Though a `factor` is an atomic vector of type `integer`, it does not test positive as an `integer`

```r
is.integer(treatment)
```

```
## [1] FALSE
```

Nor does it test positive as a `vector`

```r
is.vector(treatment)
```

```
## [1] FALSE
```

The problem is that `is.vector()` returns `TRUE` only if its argument is a vector **and** it has no attributes except (possibly) a `names` attribute.

```r
names(treatment)
```

```
## NULL
```

It is a `factor`

```r
is.factor(treatment)
```

```
## [1] TRUE
```

Data structures in R – factors

A factor could be coerced to a vector

```r
as.vector(treatment)
```

```
## [1] "a" "b" NA  "b" "a" "c" "c" "a" "b"
```

```r
typeof(treatment)
```

```
## [1] "integer"
```

but loses the `levels` information. Combining `factors` will perform a similar coercion:

```r
c(treatment)
```

```
## [1]  1  2 NA  2  1  3  3  1  2
```

```r
is.integer(c(treatment))
```

```
## [1] TRUE
```

Data structures in R – accidental factors

Often, we read in data from, say, a `.csv` file where we might be expecting only numerical values. For example, the `csv` file might have contents like this:

```
x, y
5, 3
7, -
8, 2
```

The dash " – " is a mistake in coding the data, or perhaps codes missing data. Read in (using `read.csv()`), the result assigned to `data`:

```
# for example
data <- read.csv(path_concat(dataDirectory, "fake.csv"),  header = TRUE,  sep=",")
```

the dash - will be located in the same place in `data`.

```
data
```

```
##   x y
## 1 5 3
## 2 7 -
## 3 8 2
```

Where we might have expected a numeric atomic vector, `data$y` is a `factor` (Why?)

```
data$y
```

```
## [1] 3 - 2
## Levels: - 2 3
```

Data structures in R – matrices and arrays

An atomic vector can be made to act like a matrix (or array) by simply adding an attribute `dim` to record the matrix (or array) dimensions.

```
x <- 1:12
dim(x) <- c(2,6)
x
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,]    1    3    5    7    9   11
## [2,]    2    4    6    8   10   12
```

```
class(x)
```

```
## [1] "matrix"
```

```
attributes(x)
```

```
## $dim
## [1] 2 6
```

```
typeof(x)
```

```
## [1] "integer"
```

```
length(x)
```

```
## [1] 12
```

Data structures in R – matrices and arrays

An atomic vector can be made to act like a matrix (or array) by simply adding a attribute `dim` to record the matrix (or array) dimensions.

```r
x <- 1:12
dim(x) <- c(2,3,2)
x
```

```
## , , 1
##
##      [,1] [,2] [,3]
## [1,]    1    3    5
## [2,]    2    4    6
##
## , , 2
##
##      [,1] [,2] [,3]
## [1,]    7    9   11
## [2,]    8   10   12
```

```r
class(x)
```

```
## [1] "array"
```

```r
attributes(x)
```

```
## $dim
## [1] 2 3 2
```

Data structures in R – matrices and arrays

There are also special constructor functions

```
# for matrices
x <- matrix(1:4, nrow = 3, ncol = 4)
x
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    1    4    3    2
## [2,]    2    1    4    3
## [3,]    3    2    1    4
```

```
dim(x)
```

```
## [1] 3 4
```

```
c(nrow(x), ncol(x))
```

```
## [1] 3 4
```

```
length(x)
```

```
## [1] 12
```

Data structures in R – matrices and arrays

There are also special constructor functions

```
# For arrays
y <- array(1:8, dim = c(2,3,2))
y
```

```
## , , 1
##
##      [,1] [,2] [,3]
## [1,]    1    3    5
## [2,]    2    4    6
##
## , , 2
##
##      [,1] [,2] [,3]
## [1,]    7    1    3
## [2,]    8    2    4
```

```
dim(y)
```

```
## [1] 2 3 2
```

```
c(nrow(y), ncol(y))
```

```
## [1] 2 3
```

```
length(y)
```

```
## [1] 12
```

Data structures in R – matrices and arrays

Again, these are atomic vectors

```
y <- array(1:6, dim = c(2,3,2))
is.atomic(y)
```

```
## [1] TRUE
```

```
length(y)
```

```
## [1] 12
```

```
typeof(y)
```

```
## [1] "integer"
```

```
attributes(y)
```

```
## $dim
## [1] 2 3 2
```

```
is.vector(y) # explain this result
```

```
## [1] FALSE
```

Data structures in R – matrices and arrays

Subsetting

```
x
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    1    4    3    2
## [2,]    2    1    4    3
## [3,]    3    2    1    4
```

```
x[c(1,2), c(2,4)]
```

```
##      [,1] [,2]
## [1,]    4    2
## [2,]    1    3
```

```
x[c(T,F,T), c(F,T,T,F)]
```

```
##      [,1] [,2]
## [1,]    4    3
## [2,]    2    1
```

```
x[-2,]
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    1    4    3    2
## [2,]    3    2    1    4
```

```
x[2,]
```

```
## [1] 2 1 4 3
```

Data structures in R – matrices and arrays

Dimensions are dropped by default:

```
x
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    1    4    3    2
## [2,]    2    1    4    3
## [3,]    3    2    1    4
```

```
x[2,]
```

```
## [1] 2 1 4 3
```

```
dim(x[2,])
```

```
## NULL
```

```
x[2,, drop = FALSE]  # preserve the dimensions
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    2    1    4    3
```

```
dim(x[2,, drop = FALSE])
```

```
## [1] 1 4
```

Data structures in R – matrices and arrays

Matrices/arrays are still indexable as vectors:

```
x
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    1    4    3    2
## [2,]    2    1    4    3
## [3,]    3    2    1    4
```

```
x[7]
```

```
## [1] 3
```

```
x[-7]
```

```
##  [1] 1 2 3 4 1 2 4 1 2 3 4
```

```
x[[5]]
```

```
## [1] 1
```

See `help("[[")` for details.

Data structures in R – matrices and arrays

Subsetting is same on arrays

```r
y
```

```
## , , 1
##
##      [,1] [,2] [,3]
## [1,]    1    3    5
## [2,]    2    4    6
##
## , , 2
##
##      [,1] [,2] [,3]
## [1,]    1    3    5
## [2,]    2    4    6
```

```r
y[1,2,1, drop=FALSE]
```

```
## , , 1
##
##      [,1]
## [1,]    3
```

```r
y[1,2,]
```

```
## [1] 3 3
```

```r
y[,-2,1]
```

```
##      [,1] [,2]
## [1,]    1    5
## [2,]    2    6
```

Data structures in R *– matrices and arrays*

The transpose `t()` switches the rows and columns of a matrix. That is it permutes the indices:

```
x
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    1    4    3    2
## [2,]    2    1    4    3
## [3,]    3    2    1    4
```

```
t(x)
```

```
##      [,1] [,2] [,3]
## [1,]    1    2    3
## [2,]    4    1    2
## [3,]    3    4    1
## [4,]    2    3    4
```

Data structures in R – matrices and arrays

For arrays, `aperm()` can be used to permute indices:

```
y
```

```
## , , 1
##
##      [,1] [,2] [,3]
## [1,]    1    3    5
## [2,]    2    4    6
##
## , , 2
##
##      [,1] [,2] [,3]
## [1,]    1    3    5
## [2,]    2    4    6
```

```
aperm(y, perm = c(2,1,3))
```

```
## , , 1
##
##      [,1] [,2]
## [1,]    1    2
## [2,]    3    4
## [3,]    5    6
##
## , , 2
##
##      [,1] [,2]
## [1,]    1    2
## [2,]    3    4
## [3,]    5    6
```

Data structures in R – matrices and arrays

Just as vectors are combined with `c()`, conformable matrices can be combined using `cbind()` and `rbind()` (column and row binding).

```
x
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    1    4    3    2
## [2,]    2    1    4    3
## [3,]    3    2    1    4
```

```
cbind(x, 11:13, x[,3:4])
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7]
## [1,]    1    4    3    2   11    3    2
## [2,]    2    1    4    3   12    4    3
## [3,]    3    2    1    4   13    1    4
```

```
rbind(x, 11:14)
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    1    4    3    2
## [2,]    2    1    4    3
## [3,]    3    2    1    4
## [4,]   11   12   13   14
```

Data structures in R – matrices and arrays

An exception to conformable matrices when using `cbind()` and `rbind()` is the case when one of the arguments is a scalar.

```
x
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    1    4    3    2
## [2,]    2    1    4    3
## [3,]    3    2    1    4
```

```
cbind(x, 1000, x)
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9]
## [1,]    1    4    3    2 1000    1    4    3    2
## [2,]    2    1    4    3 1000    2    1    4    3
## [3,]    3    2    1    4 1000    3    2    1    4
```

Data structures in R – matrices and arrays

Similarly for arrays, the combine constructor `abind()` (from the package `abind`) is available to extend an array along different dimensions

```
library(abind)
abind(x, 11:13, x[,3:4], along = 2)
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7]
## [1,]    1    4    3    2   11    3    2
## [2,]    2    1    4    3   12    4    3
## [3,]    3    2    1    4   13    1    4
```

```
abind(y, 100 * x[c(2,3),c(3:4)], along = 2)
```

```
## , , 1
##
##      [,1] [,2] [,3] [,4]
## [1,]    1    3    5  400
## [2,]    2    4    6  100
##
## , , 2
##
##      [,1] [,2] [,3] [,4]
## [1,]    1    3    5  300
## [2,]    2    4    6  400
```

Note that the default `along` is the last dimension and `along = 0` will create at new dimension at the front.

Data structures in R – matrices and arrays

Can also give names to the rows and columns of a matrix

```
rownames(x) <- c("A", "B", "C")
colnames(x) <- c("one", "two", "three", "four")
x
```

```
##   one two three four
## A   1   4     3    2
## B   2   1     4    3
## C   3   2     1    4
```

```
x[c("A"), c("one", "three")]
```

```
##   one three
##     1     3
```

```
x[c("A"), c("one", "three"), drop = FALSE]
```

```
##   one three
## A   1     3
```

```
x[-1, c("one", "three")]
```

```
##   one three
## B   2     4
## C   3     1
```

Note that `x[-c("A"), c("one", "three")]` will fail. Negation requires numerical indices (or logicals).

Data structures in R – matrices and arrays

Can also give names to the dimensions of an array

```
dimnames(y) <- list(c("row 1", "row 2"),
                    c("col 1", "col 2", "col 3"),
                    c("slice 1", "slice 2"))
y
```

```
## , , slice 1
##
##       col 1 col 2 col 3
## row 1     1     3     5
## row 2     2     4     6
##
## , , slice 2
##
##       col 1 col 2 col 3
## row 1     1     3     5
## row 2     2     4     6
```

```
str(y)
```

```
##  int [1:2, 1:3, 1:2] 1 2 3 4 5 6 1 2 3 4 ...
##  - attr(*, "dimnames")=List of 3
##   ..$ : chr [1:2] "row 1" "row 2"
##   ..$ : chr [1:3] "col 1" "col 2" "col 3"
##   ..$ : chr [1:2] "slice 1" "slice 2"
```

`dimnames(x)` will also work.

Data structures in R – Data frames

A data frame is a list of equal-length vectors:

```
data <- data.frame(x = 1:3, y = 4:6, z=c("one", "two", "three"))
str(data)
```

```
## 'data.frame':    3 obs. of  3 variables:
##  $ x: int  1 2 3
##  $ y: int  4 5 6
##  $ z: Factor w/ 3 levels "one","three",..: 1 3 2
```

Note that the strings are turned into factors. This can be suppressed:

```
data_nofactor <- data.frame(x = 1:3, y = 4:6, z=c("one", "two", "three"),
                            stringsAsFactors = FALSE)
str(data_nofactor)
```

```
## 'data.frame':    3 obs. of  3 variables:
##  $ x: int  1 2 3
##  $ y: int  4 5 6
##  $ z: chr  "one" "two" "three"
```

A data frame can be thought of as a rectangular structure where each column is a variate and each row an observation. So it is similar to (but not the same as) a matrix.

Data structures in R – Data frames

As a rectangular structure, a data frame behaves much like a matrix and, being a list, behaves much like one of those. Consider **selection** operators

```r
data
```

```
##   x y     z
## 1 1 4   one
## 2 2 5   two
## 3 3 6 three
```

```r
data[1,]
```

```
##   x y   z
## 1 1 4 one
```

```r
data[,"x"]
```

```
## [1] 1 2 3
```

```r
data$z
```

```
## [1] one   two   three
## Levels: one three two
```

Data structures in R – Data frames

As a rectangular structure, combining (and other matrix operators) should work. Effect of adding observations (rows).

```r
data
```

```
##   x y     z
## 1 1 4   one
## 2 2 5   two
## 3 3 6 three
```

```r
moredata <- rbind(data, data[2,], c(1:(ncol(data)-1), "four"))
```

```
## Warning in `[<-.factor`(`*tmp*`, ri, value = "four"): invalid factor level, NA
## generated
```

```r
moredata
```

```
##    x y     z
## 1  1 4   one
## 2  2 5   two
## 3  3 6 three
## 21 2 5   two
## 5  1 2  <NA>
```

```r
rownames(moredata)
```

```
## [1] "1"  "2"  "3"  "21" "5"
```

Notes: 1. coercion and warning for the last row, and 2. fourth row name.

Data structures in R – Data frames

Adding variates (columns).

```
data
```

```
##   x y     z
## 1 1 4   one
## 2 2 5   two
## 3 3 6 three
```

```
moredata <- cbind(data, 100 * data, new = 1000)
```

```
## Warning in Ops.factor(left, right): '*' not meaningful for factors
```

```
moredata
```

```
##   x y     z   x   y  z  new
## 1 1 4   one 100 400 NA 1000
## 2 2 5   two 200 500 NA 1000
## 3 3 6 three 300 600 NA 1000
```

```
colnames(moredata)
```

```
## [1] "x"   "y"   "z"   "x"   "y"   "z"   "new"
```

```
moredata$x
```

```
## [1] 1 2 3
```

Notes: 1. warning for multiplication, and 2. effect on column names.

Data structures in R – Data frames

Data frames are vectors

```
data
```

```
##   x y     z
## 1 1 4   one
## 2 2 5   two
## 3 3 6 three
```

```
attributes(data)
```

```
## $names
## [1] "x" "y" "z"
##
## $class
## [1] "data.frame"
##
## $row.names
## [1] 1 2 3
```

```
length(data)
```

```
## [1] 3
```

```
typeof(data)
```

```
## [1] "list"
```

Data structures in R – Data frames

Data frames are lists

```
data
```

```
##   x y     z
## 1 1 4   one
## 2 2 5   two
## 3 3 6 three
```

```
class(data)
```

```
## [1] "data.frame"
```

```
is.data.frame(data)
```

```
## [1] TRUE
```

```
is.list(data)
```

```
## [1] TRUE
```

```
is.vector(data)  # why?
```

```
## [1] FALSE
```

Data structures in R – Data frames

Data frames are lists

```r
data
```

```
##   x y     z
## 1 1 4   one
## 2 2 5   two
## 3 3 6 three
```

```r
data[1]
```

```
##   x
## 1 1
## 2 2
## 3 3
```

```r
data$x
```

```
## [1] 1 2 3
```

```r
data[[1]]
```

```
## [1] 1 2 3
```

As a list, we might want to introduce some hierarchical structure.

Data structures in R – Data frames

Provided they have the same length, each variate/component can be any atomic vector or list.

```r
data_zAsList <- data.frame(x = 1:3, y = 4:6, z=list(1:3, 4:6, 7:9))
str(data_zAsList)
```

```
## 'data.frame':    3 obs. of  5 variables:
##  $ x    : int  1 2 3
##  $ y    : int  4 5 6
##  $ z.1.3: int  1 2 3
##  $ z.4.6: int  4 5 6
##  $ z.7.9: int  7 8 9
```

But there is a problem.

The data frame has 5 instead of 3 variates.

The problem is that `data.frame()` interprets, as separate variates/components, each and every element of any component appearing as a `list` argument to `data.frame()`.

Data structures in R – Data frames

The same thing can happen when the component/variate/column is a matrix or array.

```
data_zAsList <- data.frame(x = 1:3, y = 4:6, z = (matrix(1:12, nrow=3)))
str(data_zAsList)
```

```
## 'data.frame':    3 obs. of  6 variables:
##  $ x  : int  1 2 3
##  $ y  : int  4 5 6
##  $ z.1: int  1 2 3
##  $ z.2: int  4 5 6
##  $ z.3: int  7 8 9
##  $ z.4: int  10 11 12
```

Again, the data frame has 6 instead of 3 variates.

Data structures in R – Data frames

This can get you into trouble if elements of the list have different lengths.

```
data_zAsList <- data.frame(x = 1:3, y = 4:6, z=list(1:3, 4:5, 6:9))

Error in (function (..., row.names = NULL,
                    check.rows = FALSE,
                    check.names = TRUE,   :
  arguments imply differing number of rows: 3, 2, 4
```

There are two solutions to this problem.

1. Use the “inhibit” function `I()` to stop `data.frame()` from processing the `z` list
2. Attach the `z` list to the `data.frame()` after it has been constructed.

Data structures in `R` *– Data frames*

1. The “inhibit” function `I()` prepends the “AsIs” class to the object’s class. This stops its argument from being evaluated as its original class.

```
data_zAsList <- data.frame(x = 1:3, y = 4:6, z = I(list(1:3, 4:5, 6:9)))
str(data_zAsList)
```

```
## 'data.frame':    3 obs. of  3 variables:
##  $ x: int  1 2 3
##  $ y: int  4 5 6
##  $ z:List of 3
##   ..$ : int  1 2 3
##   ..$ : int  4 5
##   ..$ : int  6 7 8 9
##   ..- attr(*, "class")= chr "AsIs"
```

Data structures in R *– Data frames*

The effect when the component/variate/column is a matrix or array:

```r
data_zAsList <- data.frame(x = 1:3, y = 4:6, z = I(matrix(1:12, nrow=3)))
str(data_zAsList)
```

```
## 'data.frame':	3 obs. of  3 variables:
##  $ x: int  1 2 3
##  $ y: int  4 5 6
##  $ z: 'AsIs' int [1:3, 1:4] 1 2 3 4 5 6 7 8 9 10 ...
```

Data structures in R – Data frames

Or,

2. first create the data frame, and then add each list as a new component:

```r
data_zAsList <- data.frame(x = 1:3, y = 4:6)
data_zAsList$z <- list(1:3, 4:5, 6:9)
str(data_zAsList)
```

```
## 'data.frame':    3 obs. of  3 variables:
##  $ x: int  1 2 3
##  $ y: int  4 5 6
##  $ z:List of 3
##   ..$ : int  1 2 3
##   ..$ : int  4 5
##   ..$ : int  6 7 8 9
```

Data structures in R – Data frames

This is more likely to arise when the rows/observations have more structure. For example, suppose each observation is a fitted model:

```r
fit2cars <- data.frame(poly_degree = 1:3)
rownames(fit2cars) <- c("linear", "quadratic", "cubic")
fit2cars$fit_info <- lapply(fit2cars$poly_degree,
                       FUN = function(p){
                         fit <- lm(dist ~ poly(speed, p), data = cars)
                         results <- summary(fit)$coefficients
                         df <- data.frame(coefficients = results[,"Estimate"],
                                         p_values = round(results[,"Pr(>|t|)"],5)
                         )
                         df}
                       )

str(fit2cars)
```

```
## 'data.frame':    3 obs. of  2 variables:
##  $ poly_degree: int  1 2 3
##  $ fit_info   :List of 3
##   ..$ :'data.frame': 2 obs. of  2 variables:
##   .. ..$ coefficients: num  43 146
##   .. ..$ p_values    : num  0 0
##   ..$ :'data.frame': 3 obs. of  2 variables:
##   .. ..$ coefficients: num  43 146 23
##   .. ..$ p_values    : num  0 0 0.136
##   ..$ :'data.frame': 4 obs. of  2 variables:
##   .. ..$ coefficients: num  43 145.6 23 13.8
##   .. ..$ p_values    : num  0 0 0.137 0.369
```

Data structures in R – Data frames

Then the value of the `fit_info` each observation is a fitted model

```
fit2cars
```

```
##           poly_degree
## linear              1
## quadratic           2
## cubic               3
##                                                                       fit_info
## linear                                          42.9800, 145.5523, 0.0000, 0.0000
## quadratic                  42.98000, 145.55226, 22.99576, 0.00000, 0.00000, 0.13640
## cubic     42.98000, 145.55226, 22.99576, 13.79688, 0.00000, 0.00000, 0.13727, 0.36892
```

```
fit2cars$fit_info
```

```
## [[1]]
##                coefficients p_values
## (Intercept)         42.9800        0
## poly(speed, p)     145.5523        0
##
## [[2]]
##                 coefficients p_values
## (Intercept)          42.98000   0.0000
## poly(speed, p)1     145.55226   0.0000
## poly(speed, p)2      22.99576   0.1364
##
## [[3]]
##                 coefficients p_values
## (Intercept)          42.98000  0.00000
## poly(speed, p)1     145.55226  0.00000
## poly(speed, p)2      22.99576  0.13727
## poly(speed, p)3      13.79688  0.36892
```

Examining the data structure

There are a few ways which you might use to examine the data structure.

Two we have already seen.

1. the printed representation which appears in the console (via `print()`) as

```
x <- 1:10
x
```

```
##  [1]  1  2  3  4  5  6  7  8  9 10
```

```
# or equivalently as
print(x)
```

```
##  [1]  1  2  3  4  5  6  7  8  9 10
```

2. or if we want to see the structure of the object, we use `str()`

```
str(x)
```

```
##  int [1:10] 1 2 3 4 5 6 7 8 9 10
```

which reveals the detailed structure of the object. This is particularly important (as we have already seen) for more complex objects such as those constructed using `list()`.

Examining the data structure - `print()`

Note that `print()` is a **generic** function and is typically specialized according to the `class()` of the data structure.

```r
# vector
print(seq(from = 2, to = 50, by = 10))
```

```
## [1]  2 12 22 32 42
```

```r
# matrix
x <- matrix(rnorm(1000), nrow = 200)
print(head(x))
```

```
##            [,1]      [,2]       [,3]       [,4]       [,5]
## [1,]  0.3088521 -1.013707  0.3869193 -1.4895012 -1.3099636
## [2,]  0.5378807 -1.399676 -0.6360947 -1.6821909  1.8251058
## [3,] -0.4611291 -1.375043 -0.2410696  0.6945442 -0.9068607
## [4,] -0.2496483 -1.142924  0.5998035  0.4235241  0.2790625
## [5,] -0.3999582 -1.481012 -0.7976473 -1.0203408 -0.7231094
## [6,]  2.0965151  1.155833 -0.8521571 -1.4092708  0.4136341
```

```r
# array
x <- array(rnorm(1000), dim = c(20,5,10))
print(head(x))
```

```
## [1]  1.70249924  0.12435219  0.03221932  2.21592610 -0.26641531 -0.79918816
```

In each case, try just `print(x)` (or just `x`) (There is also a `tail()` function.)

Examining the data structure - print()

```r
# data frame
print(head(mtcars))
```

```
##                    mpg cyl disp  hp drat    wt  qsec vs am gear carb
## Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
## Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
## Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
## Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
## Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
## Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

```r
# a list
print(head(list(A = 1:3, b = LETTERS[1:4],
                c = list(d = letters[10:12], e = month.abb[1:3]))))
```

```
## $A
## [1] 1 2 3
##
## $b
## [1] "A" "B" "C" "D"
##
## $c
## $c$d
## [1] "j" "k" "l"
##
## $c$e
## [1] "Jan" "Feb" "Mar"
```

Examining the data structure - `print()`

```
#  A fitted model
x <- lm(mpg ~ wt + poly(disp,3), data = mtcars)
print(x)
```

```
##
## Call:
## lm(formula = mpg ~ wt + poly(disp, 3), data = mtcars)
##
## Coefficients:
##    (Intercept)                wt  poly(disp, 3)1  poly(disp, 3)2  poly(disp, 3
##         24.250            -1.293         -22.186           9.211          -7.4
```

Exercise: What happens when you call `print.default(x)` in this case?

Note: `print()` prints its value and returns it "invisibly" (i.e. doesn't return it unless it is actually assigned – see `?invisible`).

S3 classes, `print()`, and class names

The `print()` function is implemented via numerous **S3 methods** such as `print.default()`, `print.data.frame()`, and `print.lm()` (the last is from the `stats` package) which are specialized by the `class()` of the first argument matching the function name after the first dot `.`.

Structures in `R` have an associated **S3 class** accessible via `class()`. This is the most prevalent (and basic) kind of class in `R`

Try the following:

```r
#  A fitted model
x <- lm(mpg ~ wt + poly(disp,3), data = mtcars)
class(mtcars)
class(mtcars$mpg)
class(x)
class(lm)
```

Generic functions (like `print()`) can be implemented to dispatch on the class of some argument (typically the first argument) via methods which are functions of the same name appended by a “dot” and then class name.

S3 classes, `print()`, and class names

For example, we can introduce the generic function `foo()` as follows

```r
#  A generic function
foo <- function(x, y) {
    UseMethod("foo", x)
}

foo.default <- function(x, y){
    x
}

foo.data.frame <- function(x, y) {
   y
}
foo(3, 4)
foo(mtcars, 4)
foo(3, mtcars)
```

Note: Could have dispatched on `y` instead (though this is not typical in `R`)

Examining the data structure - RStudio's `View()`

In `RStudio` there is also a very useful function called `View()` which can be used to examine the value of any structure. For example, try

```r
#  A fitted model
x <- lm(mpg ~ wt + poly(disp,3), data = mtcars)
View(mtcars)
View(mtcars$mpg)
View(x)
View(lm)
```

Examining the data structure - summary()

It is often convenient to get a quick summary of data structure. To this end, `R` provides the **S3 generic function** `summary()`.

```
#  A data frame
summary(mtcars)
```

```
##       mpg             cyl             disp             hp       
##  Min.   :10.40   Min.   :4.000   Min.   : 71.1   Min.   : 52.0  
##  1st Qu.:15.43   1st Qu.:4.000   1st Qu.:120.8   1st Qu.: 96.5  
##  Median :19.20   Median :6.000   Median :196.3   Median :123.0  
##  Mean   :20.09   Mean   :6.188   Mean   :230.7   Mean   :146.7  
##  3rd Qu.:22.80   3rd Qu.:8.000   3rd Qu.:326.0   3rd Qu.:180.0  
##  Max.   :33.90   Max.   :8.000   Max.   :472.0   Max.   :335.0  
##       drat             wt             qsec             vs        
##  Min.   :2.760   Min.   :1.513   Min.   :14.50   Min.   :0.0000  
##  1st Qu.:3.080   1st Qu.:2.581   1st Qu.:16.89   1st Qu.:0.0000  
##  Median :3.695   Median :3.325   Median :17.71   Median :0.0000  
##  Mean   :3.597   Mean   :3.217   Mean   :17.85   Mean   :0.4375  
##  3rd Qu.:3.920   3rd Qu.:3.610   3rd Qu.:18.90   3rd Qu.:1.0000  
##  Max.   :4.930   Max.   :5.424   Max.   :22.90   Max.   :1.0000  
##        am              gear            carb      
##  Min.   :0.0000   Min.   :3.000   Min.   :1.000  
##  1st Qu.:0.0000   1st Qu.:3.000   1st Qu.:2.000  
##  Median :0.0000   Median :4.000   Median :2.000  
##  Mean   :0.4062   Mean   :3.688   Mean   :2.812  
##  3rd Qu.:1.0000   3rd Qu.:4.000   3rd Qu.:4.000  
##  Max.   :1.0000   Max.   :5.000   Max.   :8.000
```

Exercise: What happens when you call `summary.default(mtcars)` in this case?

Examining the data structure - summary()

Being a generic function, summary() can be specialized to provide informative summaries appropriate to the class of the object.

```
#  A fitted model
x <- lm(mpg ~ wt + poly(disp,3), data = mtcars)
summary(x)
```

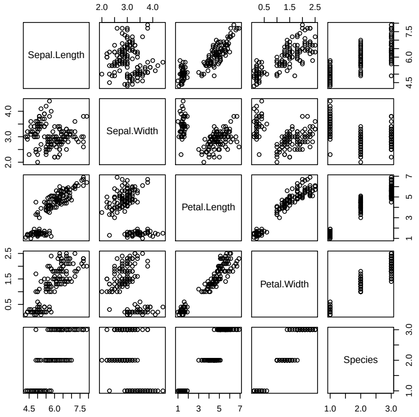
```
##
## Call:
## lm(formula = mpg ~ wt + poly(disp, 3), data = mtcars)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.9946 -1.4464 -0.3745  1.4810  4.4319
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)      24.250      4.115   5.894  2.8e-06 ***
## wt               -1.293      1.273  -1.016 0.318836
## poly(disp, 3)1  -22.186      6.547  -3.389 0.002173 **
## poly(disp, 3)2    9.211      2.223   4.143 0.000303 ***
## poly(disp, 3)3   -7.422      3.189  -2.327 0.027694 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.222 on 27 degrees of freedom
## Multiple R-squared:  0.8816, Adjusted R-squared:  0.864
## F-statistic: 50.25 on 4 and 27 DF,  p-value: 3.997e-12
```

Exercise: What happens when you call summary.default(x) in this case?

Examining the data structure - `plot()`

Finally, a visual presentation of the data can be convenient and routine. To this end, `R` provides the **S3 generic function** `plot()`.

```
#  A data frame
plot(iris)
```

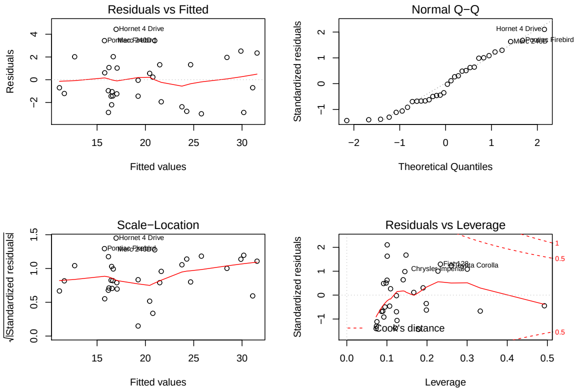


Exercise: What happens when you call `plot.default(iris)` in this case?

Examining the data structure - `plot()`

As with other **S3 generic function** `plot()` is specialized for different structures

```r
#  A fitted model
x <- lm(mpg ~ wt + poly(disp,3), data = mtcars)
par(mfrow = c(2,2))  # This will make more sense later
plot(x)
```



Exercise: What happens when you call `plot.default(x)` in this case? What does this say about default plotting?